



RESEARCH ARTICLE

Inheritance of Plant Characters Related to Insect Pest Complex in Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

The infestation of insect pests reduces crop production by 30 to 45 percent, and if preventive measures are not taken, the yield losses can exceed 70 percent. Therefore, the current study was designed to study the inheritance of cotton plant characteristics which provide the resistance against insect pests. A full diallel set of crosses were done among five cultivars of cotton viz: RH-362, VH-137, Cocker-CQ, B-598 and Karishma. All possible crosses including self and reciprocal among parents at precautionary measures and limitations to avoid contamination of genetic material at time of crossing. The F₁ population was cultivated collectively in a field using a three-replication, randomized full block design. The seeds of 20 F₁ hybrids and five parents were raised in field and data were recorded for gossypol and trichome. Genetic analysis was conducted according to the method outlined by Hayman and Jinks. The graphical representation of variance (Vr) and Co-variance (Wr) suggested over dominance type of gene action for trichomes whereas number of gossypol glands showed partial dominance of an additive gene action type.

Key words: *Gossypium hirsutum* L. over dominance; Additive genes; Trichomes and gossypol glands.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) occupies a unique and significant position in the economy of Pakistan. It is referred to be "white gold" and "life blood" for Pakistan's economy. It makes for up to 68% of our foreign exchange earnings, which is a significant portion (Zafar et al., 2024). The cotton production decreased due to some serious problem, like attack of insect pests, rainy season. Therefore, it is need to focus on Pakistan domestic cotton production in competitive demanding approach (Zafar et al., 2022). Cotton intrinsically is sensitive to a number of sucking and chewing insect pests. Among these, cotton jassid (*Amrusea devastans* Disk), Thrips (*Thrips tabaci* Lind.) and white fly (*Bemisia tabaci* Genn), the sucking insect pests were reported to cause 46% loss in yield of seed cotton (Stapule et al., 1998; Zafar et al., 2020). The statistics hve shown that due to attack of insect pest, the production of cotton yield reduced about 20 to 30

percent every year (Razzaq et al., 2021). According to a survey, 145 different bug and mite species prey on Pakistan's cotton crop (Hashmi, 1994; Zafar et al., 2020). Farmers in our nation have historically relied on insecticides to manage insect pests, much like farmers in other developing nations (Razzaq et al., 2023).

Using pesticides disturbs the crop's overall environment in addition to killing the bugs (Metcalf and Luchman, 1994). Excessive use of pesticides is not desirable at all, as it is a health hazard and also kills useful insect's predators, and increase the cost of production but besides it pollutes the environment also. According to Baloch et al. (1982), hairy cotton types were resistant to jassid attacks, whereas hairless, nectariless, and gossypol-free variants proved vulnerable to thrips and whiteflies. Additionally, a high gossypol type that was somewhat resistant to the pest of sucking insects had the highest yield (Razzaq et al., 2023). The relative loss of seed cotton yield to bollworms and jassid was examined in 11 cotton

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genotypes by Bhat et al. (1986). They found that hairiness in genotypes contributed to resistance to jassid, which caused the least amount of loss (11.96%) but was more sensitive to bollworm infestation (50.09%).

Agrawal and Karban (2000) examined the effects of constitutive and induced gland expression on two different herbivorous species: noctuid caterpillars (*Spodoptera exigua*) that chew leaves, and spider mites (*Tetranychus turkestanii*) that feed on cell content. The density of assailants had a significant impact on the induction of glands. The findings thus demonstrated that the defense mechanisms employed by cotton plants against herbivores could be broadly classified into two groups: factors not related to glands that are effective against mites and factors constitutive and inducible linked to terpenoid aldehyde-containing pigment glands that are effective against caterpillars.

The present study was conducted to determine the role of plant characters fluctuating the population of sucking insects in Upland cotton to check the resistance and to furnish genetic information related with insect resistance to produce cotton with decreased cost and in more environmentally friendly way.

MATERIALS AND METHODS

Based on variations in their phenotypic characteristics, five parents of cotton (*Gossypium hirsutum* L.) were chosen from the gene pool kept at the Plant Breeding and Genetics Department at the University of Agriculture Faisalabad, Pakistan. Experimental material comprised of a complete diallel set of crosses among four cultivars of cotton viz: RH-362, VH-137, Cocker-CQ and Karishma. The homozygosity of these parents was already maintained by the research department, further assumption was made that the inheritance of the characters would be mendelian and diploid. No, multiple allelism and reciprocal differences would be there.

Parents are grown in a glass house under controlled weather and environmental conditions e.g. temperature in the glasshouse was maintained within the range of 60° F to 90° F by using steam and electric heaters. All possible crosses including self and reciprocal among parents precautionary measures and limitations to avoid contamination of genetic material at time of crossing. A maximum of five pollinations were conducted to generate an adequate quantity of F1 seeds.

To collect self-seed, some of the buds were wrapped in butter paper bags. In June 2001, the F1

population was cultivated collectively in a field using a randomized complete block design with three replications. In order to capture the data on plant height, number of monopodial branches, number of sympodial branches, number of bolls per plant, weight of bolls, seed index, and yield of seed cotton, the seeds of 20 F1 hybrids and five parents were ear marked from each genotype. While genetic analysis was done using the methodology described by Hayman (1954) and Jinks (1955), an analysis of variance was carried out by Steel and Torrie (1981).

RESULTS AND DISCUSSION

From the breeding point of view, the availability of genetic variation is essential for the rapid and positive response to selection. Scaling tests to show the validity of the additive-dominance model for various traits in cotton (Table 1). The analysis of the F1 data revealed that there was significant variation in the number of trichomes and the number of gossypol glands (Table 2). The results of diallel analysis provided useful information about the genetic mechanism controlling the variation for these characters.

Average Number of Trichomes

Mean squares of genotypes, parents, crosses, and crosses vs. parents were highly significant. The joint regression analysis of the data on the average number of trichomes leaf showed that the regression line (0.71 ± 0.21) significantly deviated from zero ($P \leq 0.01$) and non-significantly from unity ($P \geq 0.05$) whereas the differences in arrays of both ($W_r + V_r$) and ($W_r - V_r$) were significant (Table 2). The tests suggested that model was partially adequate for genetic analysis of number of trichomes (Table 3).

The relationship between V_r and W_r was drawn to display the genetic information about the character derived from the position of the regression line. The regression line cuts W_r -axis below the origin showing over dominance (Figure 1).

Table 4 indicated that variety Karishma having maximum array mean (305.27) proved to be the best general combiner and it made the best combination with Cocker-CQ having the highest value within the array (303.93) for this trait.

Average Number of Gossypol Glands

Significant differences for all defined components except parents vs. crosses were observed (Table 2). The regression coefficient for gossypol glands ($b =$

Table 1: Scaling tests to show the validity of additive-dominance model for various traits in cotton

Sr.#	Characters	Regression analysis			Analysis of $W_r + V_r$ and $W_r - V_r$		
		b	b_0	b_1	$W_r + V_r$	$W_r - V_r$	Adequacy
1	Number of trichomes	0.716 ± 0.21	3.42 *	1.35 NS	64087255 *	4414524 **	Partially Adequate
2	Number of gossypol Glands.	0.77 ± 0.19	4.08 *	1.20 NS	17347.69 **	906.69 *	Partially Adequate

*Significant

**Highly-significant

NS: Non-Significant

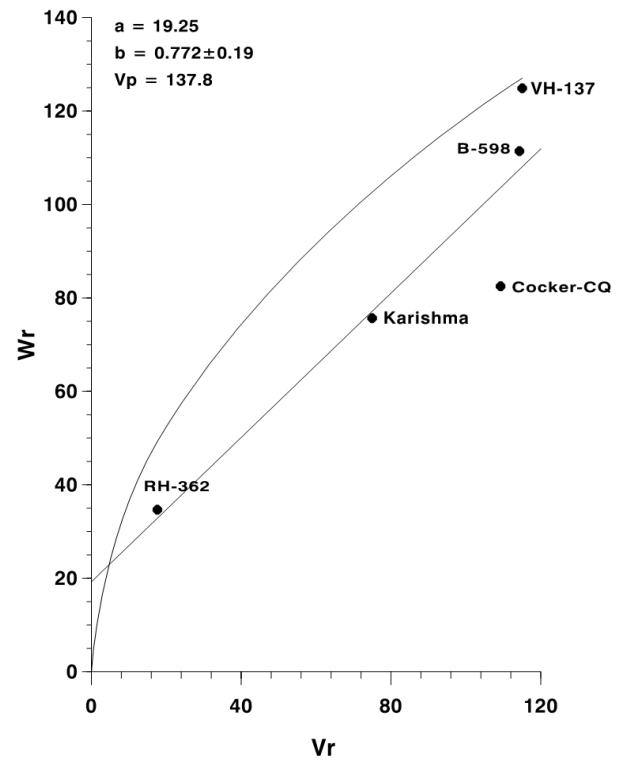
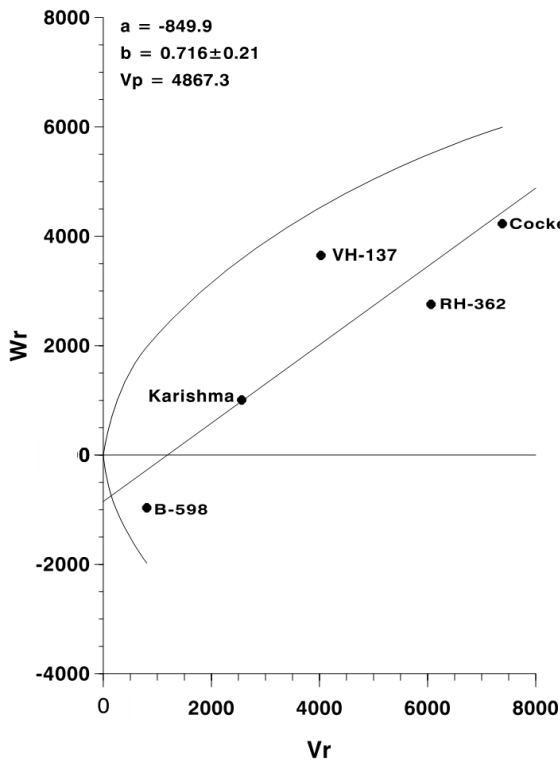


Fig 1: Vr/Wr graph of trichomes

Fig 2: Vr/Wr graph of gossypols

Table 2: Analysis of variance for W_r+V_r and W_r-V_r

Characters	Mean Squares			
	W_r+V_r Array differences (DF = 4)	W_r+V_r Block differences (DF = 10)	W_r-V_r Array differences (DF = 4)	W_r-V_r Block differences (DF = 10)
Number of trichomes	64087255**	175685.2	4414524**	46945.11
Number of Gossypol Glands	17347.69**	547.97	906.69*	268.67

* Significant ** high Significant NS non-Significant

Table 3: Analysis of variance for different traits in five cotton varieties.

Characters	Replications (DF = 2)	Genotypes (DF = 24)	Parents (DF = 4)	Crosses (DF = 19)
Number of trichomes	13.55 ^{NS}	13633.75**	14601.93**	13848.76**
Number of Gossypol Glands	13.80 ^{NS}	376.09**	413.42**	387.91**

Table 4: Mean array table of parents and F₁ hybrids for number of trichomes in cotton.

	RH-362	VH-137	Cocker-CQ	B-598	Karishma	Totals	Parents
RH-362	154.22	229.81	136.95	262.17	325.667	1108.81	154.22
VH-137	229.81	196.67	324.67	199.67	319.5	1270.3	196.67
Cocker-CQ	136.95	324.67	270.67	189	333.83	1255.11	270.67
B-598	262.17	199.67	189	206	215.33	1072.167	206
Karishma	325.67	319.5	333.93	215.33	332	1526.33	332
Totals	1108.81	1270.30	1255.11	1072.17	1526.33	6232.73	1159.55
Means	221.76	254.06	251.02	214.43	305.27	1246.55	231.91
Vars=	6062.11	4027.14	7381.58	803.83	2559.37	20734.02	4867.31
Co-vars=	2757.43	3650.67	4230.93	-966.28	1006.64	10679	

Table 5: Mean array table of parents and F₁ hybrids for gossypol glands in cotton.

	RH-362	VH-137	Cocker-CQ	B-598	Karishma	Totals	Parents
RH-362	34.2	35.2	36.98	42.9	31.73	181.01	34.2
VH-137	35.2	40.07	60.58	50.33	36.67	222.85	40.07
Cocker-CQ	36.98333	60.58333	60.66667	61.33333	53.26667	273.3333	60.67
B-598	42.9	50.33	61.83	53.47	33.67	242.2	53.47
Karishma	31.73	36.67	53.27	33.67	35.33	190.67	35.33
Totals	181.01	222.85	273.33	242.2	190.66	1110.06	223.73
Means	36.20	44.57	54.66	48.44	38.13	222.01	44.746
Vars=	17.61	115.04	109.25	114.29	74.98	431.19	137.80
Co-vars=	34.67	124.87	82.50	111.42	75.67	429.14	

0.77±0.19) departed significantly from zero, and not from unity (Table 1), which indicated the absence of non-allelic interaction. Significant differences ($P \leq 0.01$) of both (W_r+V_r) and (W_r-V_r) indicated the presence of dominance and the results of both tests suggested that simple additive dominance model was partially adequate for the gossypol glands. The graphical presentation (Fig 2) indicated partial dominance type of gene action as the line of regression passed through W_r -axis above the origin. The distribution of array points along the regression line suggested that variety RH-362 was being closest to the point of origin possessed maximum dominant genes and variety VH-137 being away from the origin possessed maximum recessive genes (Fig 2). Table 5 indicated that variety Cocker-CQ having maximum array mean (54.66) proved to be the best general combiner and it made the best combination with B-598 having the highest value within the array (61.83) for this trait.

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